

1653

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/647,978A

DATE: 06/28/2002

TIME: 11:05:41

Input Set : A:\57961.app

Output Set: N:\CRF3\06282002\I647978A.raw

3 <110> APPLICANT: Warner-Lambert Company  
 5 <120> TITLE OF INVENTION: Gene Encoding Syntaxin Interacting Protein  
 7 <130> FILE REFERENCE: 09/647,978  
 9 <140> CURRENT APPLICATION NUMBER: 09/647,978A  
 10 <141> CURRENT FILING DATE: 2000-10-06  
 12 <150> PRIOR APPLICATION NUMBER: PCT/US99/08568  
 13 <151> PRIOR FILING DATE: 1999-04-19  
 15 <150> PRIOR APPLICATION NUMBER: 60/082,454  
 16 <151> PRIOR FILING DATE: 1998-04-20  
 18 <160> NUMBER OF SEQ ID NOS: 6  
 20 <170> SOFTWARE: PatentIn Ver. 2.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1674  
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 25 <213> ORGANISM: Mouse  
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 30 aggaatgaag gaccgctgggt gtatattcat gaagtcattc ctggagggtga ctgttacaag 180  
 31 gatggacgtt tgaagccagg agatcaactt gtctcaataaa acaaggaatc tatgattgg 240  
 32 gtatcatttg aagaagcaaa aacgataatt accagagcca agttgagggtc agaatctccc 300  
 33 tgggagatag cattcatcag aaaaaagttt tacttgtggcc atccaggaaa tatttgctgt 360  
 34 ccatccccac aagtgtcaga agactgtggta cctcaaacctt caacatttac tcttcttcc 420  
 35 tctccctctg aaacactact tccaaagact tcataccactc cccagactca ggactccact 480  
 36 ttcccttctt gtaaaagcaat tcagacaaaaa cctgaacacg ataaaacaga acatagtcca 540  
 37 attacttctt tggacaacag ccctgcagat acatctaattt cagacattgc tccagcctgg 600  
 38 actgatgtatg attctggacc acaaggaaag atttccctaa atccttctgt tcgccttaag 660  
 39 gcagagaaac tggaaatggc tctcaattac ctgggtatac aqccaacaaa ggaacaacgt 720  
 40 gaagccctga gagagcaagt ccaggccgac tcaaaggaaa ctgtgtcttt tggagatttc 780  
 41 gtccaggtt ccagaagttt gtttgcttg cagttggatg aagtaaatgt tgggttccat 840  
 42 gaaatccccca gcatctttaga ctcacagctt ctccctgtt attctctaga agcagatgaa 900  
 43 gtggaaaaac ttagacaaga aagaaacgt gctctagagg aacggaatgt gcttaaggag 960  
 44 aagttaactgg aatcagaaaaa gcacaggaaa caattgtatag aagaactcca gaatgtgaag 1020  
 45 caggaagccca aagctgttagc tgaggaaacc cgagctctgc gaagccggat tcatactcgca 1080  
 46 gaagctgcac agcggcaggc acacggggat gaaatggatt atgaagaggt gatccgtctg 1140  
 47 cttagggctg aggtctcaga actaaaggtt cagctcgctg attattctga cccaaaataaa 1200  
 48 gaaagtgtcc aggacttgag aaaaagagtc accgttcttg actgccaattt gcgaaaatca 1260  
 49 gaaatggctc ggaaagccat caaggcgtcc actgaaaaggc tccttggttt catagaggct 1320  
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 53 tgcttacctt acgggtggaa ggaagcttac acagcagatg gaatcaagta cttcatcaac 1560  
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 67 Asp Pro Ala Phe Arg Val Ile Thr Val Thr Lys Glu Thr Gly Leu Gly  
     20             25                                 30  
 70 Leu Lys Ile Leu Gly Gly Ile Asn Arg Asn Glu Gly Pro Leu Val Tyr  
     35             40                                45  
 73 Ile His Glu Val Ile Pro Gly Gly Asp Cys Tyr Lys Asp Gly Arg Leu  
     50             55                                60  
 76 Lys Pro Gly Asp Gln Leu Val Ser Ile Asn Lys Glu Ser Met Ile Gly  
     65             70                                75                 80  
 79 Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg Ala Lys Leu Arg  
     80             85                                90                 95  
 82 Ser Glu Ser Pro Trp Glu Ile Ala Phe Ile Arg Gln Lys Ser Tyr Cys  
     100            105                             110  
 85 Gly His Pro Gly Asn Ile Cys Cys Pro Ser Pro Gln Val Ser Glu Asp  
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 88 Cys Gly Pro Gln Thr Ser Thr Phe Thr Leu Leu Ser Ser Pro Ser Glu  
     130            135                             140  
 91 Thr Leu Leu Pro Lys Thr Ser Ser Thr Pro Gln Thr Gln Asp Ser Thr  
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     165            170                             175  
 97 Glu His Ser Pro Ile Thr Ser Leu Asp Asn Ser Pro Ala Asp Thr Ser  
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 100 Asn Ala Asp Ile Ala Pro Ala Trp Thr Asp Asp Asp Ser Gly Pro Gln  
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 103 Gly Lys Ile Ser Leu Asn Pro Ser Val Arg Leu Lys Ala Glu Lys Leu  
     210            215                             220  
 106 Glu Met Ala Leu Asn Tyr Leu Gly Ile Gln Pro Thr Lys Glu Gln Arg  
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 109 Glu Ala Leu Arg Glu Gln Val Gln Ala Asp Ser Lys Gly Thr Val Ser  
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 112 Phe Gly Asp Phe Val Gln Val Ala Arg Ser Leu Phe Cys Leu Gln Leu  
     260            265                             270  
 115 Asp Glu Val Asn Val Gly Val His Glu Ile Pro Ser Ile Leu Asp Ser  
     275            280                             285  
 118 Gln Leu Leu Pro Cys Asp Ser Leu Glu Ala Asp Glu Val Gly Lys Leu  
     290            295                             300  
 121 Arg Gln Glu Arg Asn Ala Ala Leu Glu Glu Arg Asn Val Leu Lys Glu  
     305            310                             315                 320  
 124 Lys Leu Leu Glu Ser Glu Lys His Arg Lys Gln Leu Ile Glu Glu Leu  
     325            330                             335  
 127 Gln Asn Val Lys Gln Glu Ala Lys Ala Val Ala Glu Glu Thr Arg Ala

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128	340	345	350
130	Leu Arg Ser Arg Ile His Leu Ala Glu Ala Ala Gln Arg Gln Ala His		
131	355	360	365
133	Gly Met Glu Met Asp Tyr Glu Glu Val Ile Arg Leu Leu Glu Ala Glu		
134	370	375	380
136	Val Ser Glu Leu Lys Ala Gln Leu Ala Asp Tyr Ser Asp Gln Asn Lys		
137	385	390	395
139	Glu Ser Val Gln Asp Leu Arg Lys Arg Val Thr Val Leu Asp Cys Gln		400
140	405	410	415
142	Leu Arg Lys Ser Glu Met Ala Arg Lys Ala Phe Lys Ala Ser Thr Glu		
143	420	425	430
145	Arg Leu Leu Gly Phe Ile Glu Ala Ile Gln Glu Val Leu Leu Asp Ser		
146	435	440	445
148	Ser Ala Pro Leu Ser Thr Leu Ser Glu Arg Arg Ala Val Leu Ala Ser		
149	450	455	460
151	Gln Thr Ser Leu Pro Leu Leu Ala Arg Asn Gly Arg Ser Phe Pro Ala		
152	465	470	475
154	480	485	495
157	Thr Leu Leu Leu Glu Ser Lys Glu Leu Val Arg Ser Val Arg Ala Ile		
158	500	505	510
160	Asp Gly Ile Lys Tyr Phe Ile Asn His Val Thr Gln Thr Thr Ser Trp		
161	515	520	525
163	Ile His Pro Val Met Ser Ala Leu Asn Leu Ser Cys Ala Glu Glu Ser		
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178	ttggaaaaga agaatttcta gactcttcat caagatctc atttatacag ctgttaatc 180		
179	caaggctact ttggtaaaag catgaataaa aatacatcta ctgttagtac acccagtcta 240		
180	cttgaaaagg atcctgcctt tcagatgatt acaattgcca aggaaacagg cttggcctg 300		
181	aaggtaactag gaggaattaa ccgaaatgaa ggccattgg tatataattca ggaatttatt 360		
182	cctggaggg actgttataa ggatggcgt ttgaagccag gagatcaact tgtctcagtc 420		
183	aacaaggaat ctatgattgg ttttatcatt gaagaagcaa aaagcataat taccagagcc 480		
184	aagttgaggt tagaatctgc ttggagata gcattcataa gacaaaaatc cgacaacatt 540		
185	cagccagaaa atctgtcatg tacatcactt atagaagctt caggagaata tggaccaa 600		
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189	gcttctgcct ggactgaaaa ttatgggcta caagaaaaga tctccctaaa tccctctgtt 840		
190	cgctttaagg cagagaaaact ggaaatggct ctaaattatc ttggattca gcccacaaag 900		
191	gaacaacacc aagcccttag acagcaagta caagcagact caaaaggagc agtgtcttt 960		
192	ggagattttg tccaggttgc cagaaactt ttttgcctgc agttggatga agtaaatgtt 1020		

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 194 gcagatgaaa tggaaaggct caagtgtgaa agagatgatg ccttgaaga agtaaaataca 1140  
 195 cttaggaaaa aatttattgga atcagataag caaaggaaac aattgacaga agagctccag 1200  
 196 aatgtgaaac aagaagccaa agctgttagtt gaagaaaacaa gagccctgcg tagtcggatt 1260  
 197 catcttgctg aagctgctca gagacaggca catggaatgg aatggacta tgaagaagtg 1320  
 198 atccgtctgt tagaggccaa gattacagag ctaaaggctc agcttgcgtga ttattctgac 1380  
 199 caaaataaaag aaagtgttca ggattaaaa aagagaatca tggactcga ctgccaatta 1440  
 200 cgaaaatcg aatggctcg aaaaactttt gaggcatcca ctgaaaagct tcttcatttt 1500  
 201 gtagaggcta ttcaagaagt attttctgat aattctactc ctttatcaa tttaagtgaa 1560  
 202 agaagagctg tgtagcttc tcagacttcc ctcacaccac tggaaaggaa tggacgtac 1620  
 203 atcccagcaa cgctggcgct tgaatctaag gaacttggta aatctgtcg tgccttactt 1680  
 204 gatatggatt gtttaccta tgggtgggag gaagcttaca cagcagatgg aatcaagtac 1740  
 205 ttcatcaatc atgtaacaca gactacatcc tggatccatc cctgtatgag tgcctgaaat 1800  
 206 ctatctcgct cagaggagaa tgaagaggat tgctctagag aactccccaa ccagaaaaagt 1860  
 207 tggatgtttt ccttaggaag tggagctaca tggatgtatgt gaggcagagac gcataacatc 1920  
 208 caattcttag aatggggatc taaaatagg agttaaagcat gcactactt tggatgtgt 1980  
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 221 cggaaatgaaat gcccatttgtt atatattcag gaaattatttc ctggaggaga ctgttataag 180  
 222 gatggtcgtt tgaagccagg agatcaactt gtctcgtca acaaggaatc tatgattgg 240  
 223 gtatcatttt aagaagccaa aagcataatt accagagccaa agttgaggat agaatctgt 300  
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 231 cagcaagtac aagcagactc aaaaggggaca gtgtctttt gagattttgt ccaggttgc 780  
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 236 gctgttagtt aagaaaacaag agccctgcgt agtcggattt atcttgcgtga agctgctcg 1080  
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 238 attacagagc taaaggctca gttgtctgtat tattctgacc aaaataaaga aatgtttcg 1200  
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 250 <211> LENGTH: 553  
 251 <212> TYPE: PRT  
 252 <213> ORGANISM: Human  
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 259 20 25 30  
 261 Leu Lys Val Leu Gly Gly Ile Asn Arg Asn Glu Gly Pro Leu Val Tyr  
 262 35 40 45  
 264 Ile Gln Glu Ile Ile Pro Gly Gly Asp Cys Tyr Lys Asp Gly Arg Leu  
 265 50 55 60  
 267 Lys Pro Gly Asp Gln Leu Val Ser Val Asn Lys Glu Ser Met Ile Gly  
 268 65 70 75 80  
 270 Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg Ala Lys Leu Arg  
 271 85 90 95  
 273 Leu Glu Ser Ala Trp Glu Ile Ala Phe Ile Arg Gln Lys Ser Asp Asn  
 274 100 105 110  
 276 Ile Gln Pro Glu Asn Leu Ser Cys Thr Ser Leu Ile Glu Ala Ser Gly  
 277 115 120 125  
 279 Glu Tyr Gly Pro Gln Ala Ser Thr Leu Ser Leu Phe Ser Ser Pro Pro  
 280 130 135 140  
 282 Glu Ile Leu Ile Pro Lys Thr Ser Ser Thr Pro Lys Thr Asn Asn Asp  
 283 145 150 155 160  
 285 Ile Leu Ser Ser Cys Glu Ile Lys Thr Gly Tyr Asn Lys Thr Val Gln  
 286 165 170 175  
 288 Ile Pro Ile Thr Ser Glu Asn Ser Thr Val Gly Leu Ser Asn Thr Asp  
 289 180 185 190  
 291 Val Ala Ser Ala Trp Thr Glu Asn Tyr Gly Leu Gln Glu Lys Ile Ser  
 292 195 200 205  
 294 Leu Asn Pro Ser Val Arg Phe Lys Ala Glu Lys Leu Glu Met Ala Leu  
 295 210 215 220  
 297 Asn Tyr Leu Gly Ile Gln Pro Thr Lys Glu Gln His Gln Ala Leu Arg  
 298 225 230 235 240  
 300 Gln Gln Val Gln Ala Asp Ser Lys Gly Thr Val Ser Phe Gly Asp Phe  
 301 245 250 255  
 303 Val Gln Val Ala Arg Asn Leu Phe Cys Leu Gln Leu Asp Glu Val Asn  
 304 260 265 270  
 306 Val Gly Ala His Glu Ile Ser Asn Ile Leu Asp Ser Gln Leu Leu Pro  
 307 275 280 285  
 309 Cys Asp Ser Ser Glu Ala Asp Glu Met Glu Arg Leu Lys Cys Glu Arg  
 310 290 295 300  
 312 Asp Asp Ala Leu Lys Glu Val Asn Thr Leu Lys Glu Lys Leu Leu Glu  
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